

FIGURE 1

```
1  agcctttact  tttctttcaa  cttttcatcc  cgatactttt  ttgtaatagt  ttttttcatt
61  aataatacaa  gtcctgatit  tgcaagaata  atccttttta  gataaaaaata  tctatgctaa
121 taataacatg  taaccactta  catttaaaaa  ggagtgtat  catgttatat  ccaatcaata
181 cagaaacccg  aggagttttt  gatttaaatg  gggctctgga  ttttaaatta  gattacggca
241 aaggactgga  agaaaagtgg  tatgaatcaa  aactgacaga  taccatatca  atggctgtac
301 cttcctccta  taatgatatc  ggtgttacga  aggaaattcg  aaaccatata  ggctatgtat
361 ggtacgagcg  tgaattttacc  gttcctgctt  atttaaaaga  tcagcgcata  gtcctgcgtt
421 ttggttcagc  aacacataag  gctattgtat  acgttaacgg  agaactagta  gttgaacaca
481 aaggcggctt  cttacggttt  gaggcagaaa  taaacaacag  cttagagagc  ggaatgaatc
541 gtgtaacagt  agcgggtgat  aatatttttag  atgattctac  gctcccagtt  gggctatata
601 gtgaaagaca  tgaagaaggt  ttgggaaaag  tgattcgtaa  taaacctaat  tttgacttct
661 ttaactatgc  aggtttacat  cgtcctgtaa  aaatttatac  aacccctttt  acctatgttg
721 aggatatatc  ggttgaacc  gattttaacg  gtccaacggg  aacagttacg  tatacagttg
781 attttcaggg  taaggcagaa  accgtaaagg  ttagtgtagt  tgatgaagaa  gggaaagttg
841 ttgcttcaac  tgaaggcctc  tctggtaatg  ttgagattcc  taacgttata  ctttgggaac
901 ctttaaaatac  ctatctctat  caaattaaag  ttgagttagt  aaatgatggg  ctaactattg
961 atgtatacga  agagccattt  ggaggtcgaa  cgttggaagt  aaacgacggg  aaattcctca
1021 ttaataacaa  accattttat  tttaaagggg  tcggaaaaca  cgaggatact  ccaataaatg
1081 gaagaggctt  taatgaagaa  tcaaagttaa  tggattttaa  tattttgaaa  tggatcgggtg
1141 cgaattcctt  tcggacggcg  cactatcctt  attctgaaga  actgatgcgg  ctgcagatc
1201 gtgaagggtt  agtcgtcata  gatgaaaccc  cagcagttgg  tgttcatttg  aactttatgg
1261 caacgactgg  tttgggcgaa  ggttcagaga  gagtgaatc  ttgggaaaaa  atccggacct
1321 ttgaacatca  tcaagatgta  ctgagagagc  tgggtttctg  tgataaaaaa  caccctcttg
1381 ctgtcatgtg  gtcgattgca  aatgaagcgg  ctacggaaga  agaaggcgtt  tatgaatact
1441 ttaagccatt  agttgaatta  acgaagagat  tagatccaca  aaaacgcccc  gttaccattg
1501 ttttgttcgt  aatggcgaca  ccagaaacag  ataaagtggc  ggagttaatt  gatgtgattg
1561 cattgaatcg  atacaacggc  tggtrattttg  atgggggtga  tcttgaagcc  gcgaaagtcc
1621 accttcgtca  ggaattttat  gcgtggaata  aacgctgtcc  aggaaaaact  ataagtataa
1681 cagagtatgg  ggctgatacc  gtagctgggt  ttcattgat  tgatccgggt  atgtttacag
1741 aagagtatca  ggttgaatat  taccoagcaa  atcatgtagt  atttgatgaa  tttgagaact
1801 ttgttggcga  gcaggcctgg  aattttgcag  actttgctac  aagccagggt  gtcattgcgtg
1861 ttcaaggtaa  caaaaagggt  gttttcacac  gcgaccgcaa  accaaaatta  gcagcacatg
1921 ttttccgcga  acgttggaca  aacatcccg  atttcgggta  taaaaattaa  taaaagctg
1981 gttctccaat  aggaggccag  cttttttaca  tggatacaat  ggttgtaat  taaaacctt
2041 cttcattttt  tatataaaaa  tgaagagggt  ctttaatttt  taaatgttat  tacattttt
```

FIGURE 2

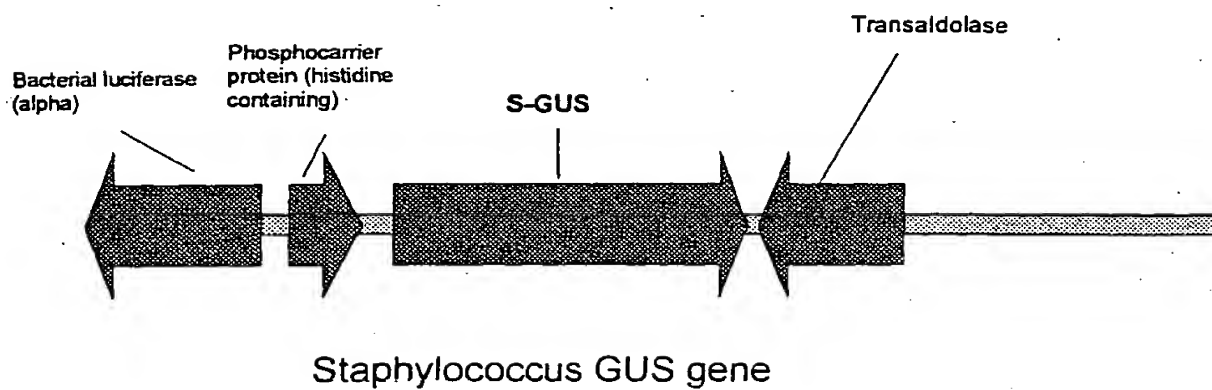


FIGURE 3A

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A

Staphylococcus β -glucuronidase

```
1  MLYPINTETR GVFDLNGVWN FKLDYGKGLE EKWYESKLTD TISMAVPSSY
51 NDIGVTKEIR NHIGYVWYER EFTVPAYLKD QRIVLRFSGA THKAIVYVNG
101 ELVVEHKGGF LPFEAEINNS LRDGMNRVTV AVDNILDDST LPVGLYSERH
151 EEGLGKVIRN KPNFDFFNIA GLHRPVKIYT TPFTYVEDIS VVTDFNGPTG
201 TVTYTVDFQG KAETVKVSVV DEEGKVFAST EGLSGNVEIP NVILWEPLNT
251 YLYQIKVELV NDGLTIDVYE EPFGVRTVEV NDGKFLINNK PFYFKGFGKH
301 EDTPINGRGF NEASNVMDFN ILKWIGANSF RTAHYPYSEE LMLADREGL
351 VVIDETPAVG VHLNFMATTG LGEGERVST WEKIRTFEHH QDVLRELVS
401 DKNHPSVVMW SIANEAAATEE EGAYEYFKPL VELTKELDPQ KRPVTIVLFV
451 MATPETDKVA ELIDVIALNR YNGWYFDGGD LEAAKVHLRQ EFHAWNKRC
501 GKPMITEYGA ADTVAGFHD I DPVMFTEEQ VEQYQANHV FDEFENFVGE
551 QAWNFADFAT SQGVMRVQGN KKGVFTRDRK PKLAAHVFRE RTNIPDFGY
601 KN
```

B

Enterobacter/Salmonella β -glucuronidase

```
1  GKLSPTPTAY IQDVTVXTDV LENTEQATVL GNVGADGDIR VELRDGQQQI
51 VAQGLGATGI FELDNPHLWE PGEGYLYELR VTCEANGECD EYPVRVGIRS
101 ITXKGEQFLI NHKPFYLTGF GRHEDADFRG KGFDPVLMVH DHALMNWIGA
151 NSYRTSHYPY AEKMLDWADE HVIVVINETA AGGFNTLSLG ITFDAGERPK
201 ELYSEEANG ETSQQAHLQA IKELIARDKN HPSVVCWSIA NEPDTRPNGA
251 REYFAPLAKA TRELDPTRPI TCVNVMFCDA ESDTITDLFD VVCLNRYYGW
301 YVQSGDLEKA EQMLEQELLA WQSKLHRPII ITEYGVDTLA GMPSVYPDMW
351 SEKYQWKWLE MYHRVFDGRS VC
```

C

Staphylococcus homini β -D-glucuronidase

```
1  GLSGNVEIPN VILWEPLNTY LYQIKVELVN DGLTIDVYEE PFGVRTVEVN
51 DGKFLINNKP FYFKGFGKHE DTPINGRGFN EASNVMDFNI LKWIGANSFR
101 TAHYPYSEEL MRLADREGLV VIDETPAVG VHLNFMATTGL GEGSERVSTW
151 EKIRTFEHHQ DVLRELVS RD KNHPSVVMWS IANEAATEEE GAYEYFKPLG
201 GAAKELDPXK RPVTIVLFVM ATPETDKVAE LIDVIALNRY NGWYFDGGDL
251 EAAKVHLRQE FHAWNKRC PG KPIMITEYGA DTVAGFHDID PVMFTEEQV
301 EYQYQANHV F DEFENFVGEQ AWFADFATS QGVMRVQGNK KGVFTRDRK
351 XLAHVFRER RTNIPDFGYK NASHHH
```

FIGURE 3B

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D

Staphylococcus warneri β -D-glucuronidase

```
1  LXMLHPITTG TRGGFALYGX XNLMLDYGXG LTDWTXSLT TELSRLVVL
51 WTHXLTGEX PAISILWPNS ELTVSXLYXG SLXSSSXLC SLTXHVVICQ
101 XVT LXVDHTG LIXXFEFMST TCCXXDELVT GTLAXILYHX ILPHGLYRKR
151 HEXGLGKXNF YXLHFAFFXY AXLXRTVXMY XNLVRXQDIX VVTXXHXXXX
201 TVEQCVXXNX KIXSVKITIL DENDHAIXES EGAKGNVTIQ NPILWQPLHA
251 YLYNMKVVELL NDNECVDVYT ERFGIRSVEV KDGQFLINDK PFYFKGFGKH
301 EDTYXNGRGL NESANVMDIN LMKWIGANSF RTSHYPYSEE MMLADEQGI
351 VVIDETTXVG IHLNFMXTLG GSXAHDTWXE FDTLEFHKEV IXDLIXRDKN
401 HAWVVMWXFG NEXGXNKGGA KAXFEPFVNL AGEKDXXXXP VTIVTILXAX
451 RNVCEVXDLV DVVCLXXXXG WYXQSGDLEG AKXALDKEXX EWWKXQXNKP
501 XMFTEYGVDX VVGLXXXPKD MXPEEYKMXF YKGYXKIMDK
```

E

Thermotoga maritima β -glucuronidase

```
1  MVRPQRNKKR FILILNGVWN LEVTSKDRPI AVPGSWNEQY QDLCYEEGPF
51 TYKTTFYVPK XLSQKHIRLY FAAVNTDCEV FLNGEKVGEN HIEYLPFEVD
101 VTGKVKSGEN ELRVVVENRL KVGGFPSKVP DSGTHTVGFF GSFPPANFDF
151 FPYGGIIRPV LIEFTDHARI LDIWVDTSES EPEKKLGKVK VKIEVSEEAV
201 GQEMTIKLGE EEKKIRTSNR FVEGEFILEN ARFWSLEDPY LYPLKVELEK
251 DEYTLDIGIR TISWDEKRLY LNGKPVFLKG FGKHEEFPVL GQGTIFYPLMI
301 KDFNLLKWIN ANSFRTSHYP YSEEWDLAD RLGILVIDEA PHVGITRYHY
351 NPETQKIAED NIRRMIDRHK NHPSVIMWSV ANEPESNHPD AEGFFKALYE
401 TANEMDRTRP VVMVSMMDAP DERTRDVALK YFDIVCVNRY YGWYIYQGRI
451 EEGLOALEKD IEELYARHRK PIFVTEFGAD AIAGIHYDPP QMFSEEQAE
501 LVEKTIRLLL KKDYIIGTHV WAFADFKTPQ NVRRPILNHK GVFTDRDQPK
551 LVAHVLRLW SEV
```

FIGURE 4A

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Staphylococcus β -glucuronidase

MetLeuTyrProIleAsnThrGluThrArgGlyValPheAspLeuAsnG1
1 ATGTTATATCCAATCAATACAGAAACCCGAGGAGTTTTTGATTAAATGG

yValTrpAsnPheLysLeuAspTyrGlyLysGlyLeuGluGluLysTrpT
51 GGTCTGGAATTTTAAATTAGATTACGGCAAAGGACTGGAAGAAAAGTGGT

yrGluSerLysLeuThrAspThrIleSerMetAlaValProSerSerTyr
101 ATGAATCAAACTGACAGATACCATATCAATGGCTGTACCTTCCTCCTAT

AsnAspIleGlyValThrLysGluIleArgAsnHisIleGlyTyrValTr
151 AATGATATCGGTGTTACGAAGGAAATTCGAAACCATATCGGCTATGTATG

pTyrGluArgGluPheThrValProAlaTyrLeuLysAspGlnArgIleV
201 GTACGAGCGTGAATTTACCGTTCCTGCTTATTTAAAAGATCAGCGCATCG

alLeuArgPheGlySerAlaThrHisLysAlaIleValTyrValAsnGly
251 TCCTGCGTTTTGGTTCAGCAACACATAAGGCTATTGTATACGTAAACGGA

GluLeuValValGluHisLysGlyGlyPheLeuProPheGluAlaGluIl
301 GAACTAGTAGTTGAACACAAAGGCGGCTTCTTACCGTTTGAGGCAGAAAT

eAsnAsnSerLeuArgAspGlyMetAsnArgValThrValAlaValAspA
351 AAACAACAGCTTAAGAGACGGAATGAATCGTGTAACAGTAGCGGTTGATA

snIleLeuAspAspSerThrLeuProValGlyLeuTyrSerGluArgHis
401 ATATTTTAGATGATTCTACGCTCCAGTTGGGCTATATAGTGAAAGACAT

GluGluGlyLeuGlyLysValIleArgAsnLysProAsnPheAspPhePh
451 GAAGAAGGTTTGGGAAAAGTGATTTCGTAATAAACCTAATTTTGACTTCTT

eAsnTyrAlaGlyLeuHisArgProValLysIleTyrThrThrProPheT
501 TAACTATGCAGGCTTACATCGTCCTGTAAAAATTTATACAACCCCTTTTA

hrTyrValGluAspIleSerValValThrAspPheAsnGlyProThrGly
551 CCTATGTTGAGGATATATCGGTTGTAACCGATTTTAACGGTCCAACGGGA

ThrValThrTyrThrValAspPheGlnGlyLysAlaGluThrValLysVa
601 ACAGTTACGTATACAGTTGATTTTCAGGGTAAGGCAGAAACCGTAAAGGT

lSerValValAspGluGluGlyLysValValAlaSerThrGluGlyLeuS
651 TAGTGTAGTTGATGAAGAAGGGAAAGTTGTTGCTTCAACTGAAGGCCTCT

FIGURE 4B

erGlyAsnValGluIleProAsnValIleLeuTrpGluProLeuAsnThr
701 CTGGTAATGTTGAGATTCCTAACGTTATCCTTTGGGAACCTTTAAATACC

TyrLeuTyrGlnIleLysValGluLeuValAsnAspGlyLeuThrIleAs
751 TATCTCTATCAAATTAAAGTTGAGTTAGTAAATGATGGTCTAACTATTGA

pValTyrGluGluProPheGlyValArgThrValGluValAsnAspGlyL
801 TGTATACGAAGAGCCATTTGGAGTTCGAACCGTTGAAGTAAACGACGGGA

ysPheLeuIleAsnAsnLysProPheTyrPheLysGlyPheGlyLysHis
851 AATTCCTCATTAAATAACAAACCATTTTATTTTAAAGGGTTCGGAAAACAC

GluAspThrProIleAsnGlyArgGlyPheAsnGluAlaSerAsnValMe
901 GAGGATACTCCAATAAATGGAAGAGGCTTTAATGAAGCATCAAATGTAAT

tAspPheAsnIleLeuLysTrpIleGlyAlaAsnSerPheArgThrAlaH
951 GGATTTTAAATATTTTGAAATGGATCGGTGCGAATTCCTTTCGGACGGCGC

isTyrProTyrSerGluGluLeuMetArgLeuAlaAspArgGluGlyLeu
1001 ACTATCCTTATTCTGAAGAACTGATGCGGCTCGCAGATCGTGAAGGGTTA

ValValIleAspGluThrProAlaValGlyValHisLeuAsnPheMetAl
1051 GTCGTCATAGATGAAACCCAGCAGTTGGTGTTTCAATTTGAACTTTATGGC

aThrThrGlyLeuGlyGluGlySerGluArgValSerThrTrpGluLysI
1101 AACGACTGGTTTGGGCGAAGGTTTCAGAGAGAGTGAGTACTTGGGAAAAAA

leArgThrPheGluHisHisGlnAspValLeuArgGluLeuValSerArg
1151 TCCGGACCTTTGAACATCATCAAGATGTACTGAGAGAGCTGGTTTCTCGT

AspLysAsnHisProSerValValMetTrpSerIleAlaAsnGluAlaAl
1201 GATAAAAACCAACCCTCTGTTGTCATGTGGTCGATTGCAAATGAAGCGGC

aThrGluGluGluGlyAlaTyrGluTyrPheLysProLeuValGluLeuT
1251 TACGAAGAAGAAGGCGCTTATGAATACTTTAAGCCATTAGTTGAATTAA

hrLysGluLeuAspProGlnLysArgProValThrIleValLeuPheVal
1301 CGAAAGAATTAGATCCACAAAAACGCCAGTTACCATTGTTTTGTTTCGTA

MetAlaThrProGluThrAspLysValAlaGluLeuIleAspValIleAl
1351 ATGGCGACACCAGAAACAGATAAAGTGGCGGAGTTAATTGATGTGATTGC

aLeuAsnArgTyrAsnGlyTrpTyrPheAspGlyGlyAspLeuGluAlaA
1401 ATTGAATCGATACAACGGCTGGTATTTTGATGGGGGTGATCTTGAAGCCG

FIGURE 4C

1aLysValHisLeuArgGlnGluPheHisAlaTrpAsnLysArgCysPro
1451 CGAAAGTCCACCTTCGTCAGGAATTTTCATGCGTGGAATAAACGCTGTCCA

GlyLysProIleMetIleThrGluTyrGlyAlaAspThrValAlaGlyPh
1501 GGAAAACCTATAATGATAACAGAGTATGGGGCTGATACCGTAGCTGGTTT

eHisAspIleAspProValMetPheThrGluGluTyrGlnValGluTyrT
1551 TCATGATATTGATCCGGTTATGTTTACAGAAGAGTATCAGGTTGAATATT

yrGlnAlaAsnHisValValPheAspGluPheGluAsnPheValGlyGlu
1601 ACCAAGCAAATCATGTAGTATTTGATGAATTTGAGAACTTTGTTGGCGAG

GlnAlaTrpAsnPheAlaAspPheAlaThrSerGlnGlyValMetArgVa
1651 CAGGCCTGGAATTTTGCAGACTTTGCTACAAGCCAGGGTGTCATGCGTGT

lGlnGlyAsnLysLysGlyValPheThrArgAspArgLysProLysLeuA
1701 TCAAGGTAACAAAAAAGGTGTTTTTCACACGCGACCGCAAACCAAATTAG

laAlaHisValPheArgGluArgTrpThrAsnIleProAspPheGlyTyr
1751 CAGCACATGTTTTCCGCGAACGTTGGACAAACATCCCGGATTTCCGGTTAT

LysAsn
1801 AAAAAT

FIGURE 4D

Enterobacter/Salmonella β -glucuronidase gene

CATTGGGGAACTTTCCCCACACCTACTGCGTATATTCAGGATGTTACG 50
GTINTTACTGATGTTTTGGAAAATACTGAACAGGCGACCGTAACTGGGGA 100
ATGTGGGGGCTGATGGTGATATTCGGGTTGAGCTTCGCGATGGGCAGCAA 150
CAAATAGTGGCACAAGGGCTGGGGGCCACAGGTATATTTGAACTGGATAA 200
TCCTCATCTTTGGGAACCAGGTGAAGGGTATTTGTACGAGCTGCGGGTTA 250
CCTGCGAAGCCAATGGTGAGTGTGACGAATATCCAGTACGTGTCSGTATC 300
CGTTCATTACGGNTAAGGGTGAGCAGTTTTTGATTAAACCACAAACCGTT 350
TTATTTAACCCGGTTTTGGTCGACATGAAGATGCAGATTTTCGCGGCAA 400
GGTTTCGACCCGGGTGTTGATGGTTCACGACCACGCGTTGATGAACTGGA 450
TTGGGCTAACTCCTATCGCACGTCCCCTACCCTTACGCGGAAAAGATGC 500
TCGATTGGGCTGATGAGCACGTATCGTAGTGATTAATGAAACCGCGGCGG 550
GTGGCTTTAACAACCTTATCGTTGGGAATCACTTTTGACGCAGGCGAAAGA 600
CCTAAAGAACTTCTACAGCGAAGAGGCGATTAATGGCGAGACTTCAGCAG 650
GCTCACTTGCAGGCTATAAAAGAGCTTATTGCCCGGGATAAAAACCATCC 700
AAGTG TAGTGTGTGGAGTATTGCCAATGAGCCCGACACCCGTCCAAATGG 750
AGCCAGAGAGTACTTTGCGCCTTTAGCTAAGGCCACTCGTGAACTGGATC 800
CGACACGTCCGATTACCTGCGTAAACGTGATGTTCTGCGATGCCGAAAGC 850
GACACCATCACCGACCTGTTGACGTGGTTTTGTCTGAATCGCTATTACGG 900
CTGGTATGTGCAATCAGGTGATTTGGAAAAGCAGAACAGATGCTGGAGC 950
AAGAACTGCTGGCCTGGCAGTCAAACTACATCGCCCAATTATTATTACG 1000
GAATACGGTGTGCGATACGCTGGCAGGAATGCCCTCGGTTTATCCCGACAT 1050
GTGGAGTGAAAAGTACCAGTGAAATGGCTTGAAATGTATCACCGTGTCTT 1100
TGACCGGGGGAGCGTTTGCAAGCGCNAAGCTTAGTTAACACCGGNGGTAC 1150
CGATCACGCGTNAGGCGCCNCCCATGNCATATGNGCTAGCNTGCGGCCG 1200

FIGURE 4E

CNATGCATTCTGCAGCGATCGCAGCTGAGTACACGAGCTCACCCGCGGAG 1250
TCGACAAGATCCAAGTACTACCCGGGNATACGTAAGTAGTGCATGCTCGC 1300
GAAATATTTAGGCCTTATCGAATTAAT 1328

Pseudomonas β -D-glucuronidase

CTTGCTGGACNACNGTTNAGGATTTTTAGACACGNGGAGCTAAAGCTTGC 50
TGACCNAACTATCACGCCGGNCGTGCANGCTTGGACCGCGACATTNCCTG 100
ACANGNGAAANACTCCGCCATATCCATCTTTGCTGGCCCAACAGTGAGTT 150
NACNGTNNCGNACNNTNNGANGGATCAGTGNATCGAGCTCCNTTNANNIT 200
CTNCGCTAACATAACATGTNGCATATGTCAATNAATNACGCTGGNCGTGG 250
ANCNCACCGGGCTNATTCGNTGNNATTGGAATTGNATGNCAACAACNTG 300
NTGCACGNTGGNAAANAATTGCGTNACAGGGACTTTGGCCNCTTCCTAAA 350
CCATNGCATCCTCCCNATGGGCTGTACACGAATGNGCCCCCAAANGGCN 400
TTCAGAAAGGCAATTTNTAACAAGGCNGANNTTTGACTTTTTCAACTATG 450
CAGNNCTGCACCGGACGCTGAAAATGTACANGACCCTGGGTACGTNCNAC 500
CAAGACATNNAAGTNGTGACCGACTCCATTGTNCTAACCGGGACTGTACC 550
TATAATGCGGACTATCANGGCAATGCATGACGTNGAANCGACACACCAGG 600
ATNAGGAAAACAANTGGTGGNANCNCACCANGCCATGATTGTCACGTTTT 650
GTTAGCNTNGANACNAATTCNATTGCTTTNTTAGCTTNTTANATNAGCCT 700
NTTTANATTAGANTTCTNANTGAGACTGT 730

Salmonella β -glucuronidase

NCTCATGACCCNCCNTTTTNGTANCNTNTTTGNNANCTGCTGCANNNGA 50
TCACNACNNGGANNCGGGGNGGGTTCGNNCTCTATGGCNCGNGGAACNNN 100
ATGNTGGNCNACNGTTNANGACTGACAGACACGTGGAGCTAAAGCTTGCT 150

FIGURE 4F

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GCCGAAGTATCACTCAGNTCNTGNAAGTTGGACAACACATTNCCTGACAN 200
GNGAAAAGCCCCGCCATATCCATACTGTGCTGGCCCAACANTGAGTTCACN 250
GTCGTGCGNACTNTATGANGGATCACCTGTATCGANCTCCNTTNATNTTCT 300
NCAGCTAACATAACTGTGNGCATATGTCAATGNATGACCTGGTCGGTGNA 350
NCACACCGGGCGTNATTGNTGNNATTGGAATTTNATGTCAACAACTTTGN 400
TGCANGNTGGAATGAATCTGGGGGCCAGGGACTTTGGCCANCTTCCTNAA 450
CCATTGCGANCCTCCCCAGTGGGCTTGTAACACNATTGNGCCCCAAAAAG 500
GCNTCAGATAGGCATTTTGACAAGCTCCANNTTAACTTTTTCAACTATGC 550
NGNCCTGCACCGGACGCTGAAAAANGTACANGANCTTGTACGTTCCACC 600
AAGANATTTAAGGTGTGACCCACNTCCATTTTCCTAACNGGACTGTGACT 650
NATAAAGGNTGACCNTTCANGGACACATTGCAATGACCCTTTNAAACGGA 700
ANAACCCCCGNTTAAAGGAAAAACAAATTTGGTTGGGNAGTCCANCCAA 750
GGGCCAATTANTTGTTCNCNGGGGGANTAAANCCCCCNCCAATCGATCTT 800
CGAAATTTAAACAGCGCTCCGGCCGCCACGTGCGAATTCCGATATCGGAT 850
GAGGCCAGCGCNAAGCTTAGTTAACACCGGNGGTACCGATCACGCGTNAG 900
GCGCCNCCCATGGNCATATGNGCTAGCNTGCGGCCGCNATGCATTCTGCA 950
GCGATCGCAGCTGAGTACACGAGCTCACCCGCGGAGTCGACAAGATCCAA 1000
GTACTACCCGGGNATACGTAAGTAGTGATGCTCGCGAAATATTTAGGCC 1050
TTATCGAATTAA 1063

Staphylococcus warneri β -glucuronidase

TANANCTTGTNTCTGCTGCACCCNATCACGACAGGGACCCGGGGNGGGTT 50
CGCGCTCTATGGCNCNGGGAACCTTAATGCTGGACTACGGTTNAGGACTGA 100
CAGACACGTGGACTNAAAGCTTGCTGACCGAACTATCACGACTGGTCGTG 150
CTAAGTTGGACCACACATTNCCTGACAGGGGAAANACCCGCCATATCCAT 200

FIGURE 4G

CTTGTGGCCCAACAGTGAGTTAACCGTGTGCGANCTTATATGANGGATCAC 250
TGNATTGAGCTCCNTCTTATGTTCTTCGCTAACATANCATGTNGTCATA 300
TGTCAATANGTGACNCTGGNCGTGGATCACACCGGGCTNATTGNTGNATT 350
CGAATTTATGTCAACAACCTTGTTGCANGNTGGATGAATTGGTNACAGGGA 400
CTTTGGCCANCATCCTATACCATNGCATCCTTCCCCATGGGCTTTACCGA 450
AAGCGCCACGAAAANGGCCTCGGAAAAGNCAATTTTTACNGGCTCCACTT 500
TGCNTTTTTCAANTATGCNGANCTGNACCGGACGGTNANAATGTACANGA 550
ACCTTGACGTCNNCAAGACATTTAGGTTGTGACCGNTTAGCATNAGCNG 600
TNNTAAACAGTAGAACAATGTGTGANCCNTAACTAAAAAATANACAGCGT 650
TAAATCACGATTCTGGATGAAAATGATCATGCAATANCCGAAAGCGAAG 700
GCGCTAAAGGCAATGTAAC TATTCAAATCCTATATTGTGGCAACCTTTA 750
CATGCCTATTTATACAATATGAAAGTAGAATTACTCAACGATAATGAGTG 800
TG TAGATGTTTATACAGAACGTTTCGGTATTTCGATCTGNGAAGTGAAGG 850
ATGGACAGTTTTTAATTAATGACAAACCATTTTATTTCAAAGGTTTCGGT 900
AAACATGAAGATACCTATTAAAATGGTCGAGGCTTAAACGAATCAGCCAA 950
CGTCATGGACATCAACTTAATGAAATGGATAGGTGCTAATTCATTTAGAA 1000
CCTCTCATTACCCATATT CAGAAGAAATGATGCGTTTAGCAGATGAACAA 1050
GGTATTGTAGTGATAGATGAGACAACANGTGTGCGGTATACATCTTAATTT 1100
TATGGNNACCTTAGGTGGCTCCNTTGACATGATACATGGAANGAATTTG 1150
ACACTCTCGAGTTTCATAAAGAAGTCATANAAGACTTGATTGNGAGAGAC 1200
AAGAATCATGCATGGGTAGTCATGTGGTNATTTGGCAATGAGCNAGGGTN 1250
AAATAAAGGGGGTGCTAAAGCATNCTTTGAGCCATTTGTTAATTTAGCAG 1300
GTGAAAAAGATNNTCNGNNTNGCCAGTGACTATCGTTACTATATTANCT 1350
GCNNANCGAAATGTATGTGAAGTTNNAGATTTAGTCGATGTGGTTTGTCT 1400

FIGURE 4H

NNNNAGNNNTANGGTTGGTATNCACAATCAGGTGATTTAGAAGGTGCTA 1450
AACNAGCATTAGATAAGGAGNTAGNCGAATGGTGGAAANGACAACNAAAT 1500
AAGCCAATNATGTTTACAGAGTATGGTGTGGATANNGTTGTAGGTTTACA 1550
NNCGATNCCTGATAAAATGCNNCCAGAAGAGTATAAAATGAGNTTTTATA 1600
AAGGNTATNATAAAATTATGGATAAACGATCGCAGCTGAGTACACGAGCT 1650
CACCCGCGGAGTCGACAAGATCCAAGTACTACCCGGGNATACGTAACTAG 1700
TGCATGCTCGCGAAATATTTAGGCCTTATCGAATTAAT 1739

Staphylococcus homini β -glucuronidase gene

TGTGGGNCTTTGTTTCCTTGNTCAGCTCCCCAACGGCTTGAAGTACTCGTA 50
CGCGCCCTCTTCCTCAGTCGCCGCCTCGTTGGCGATGCTCCACATCACGA 100
CGCTTGGATGGTTCTTGTACGAGACACCAGTTCACGGAGAACGTCTTGA 150
TGGTGCTCAAACGTCCGAATCTTCTCCCAGGTACTGACGCGCTCGCTGCC 200
TTCGCCGAGTCCCGTGGTGGCCATGAAGTTGAGGTGCACGCCAACTGCCG 250
GAGTCTCGTCGATCACGACCAGACCCTCGCGATCCGCAAGACGCATCAAC 300
TCTTCAGAGTACGGATAGTGTGCGGTCCGGAAGCTGTTGGCGCCGATCCA 350
TTTGAGGATATTGAAATCCATCACATTGCTCGCTTCGTTAAAGCCACGGC 400
CGTTGATAGGAGTGTCTCATGTTTGCCAAAGCCCTTGAAGTAGAACGGT 450
TTGTTGTTGATGAGGAACTTGCCGTCGTTGACTTCACGGTCCGCACGCCG 500
AACGGCTCTTCATAGACATCGATGGTCAAGTCCCGTCGTTACCAAGTTCC 550
ACTTTGATCTGGTAGAGATACGTGTTCAAGTGGTTCCCAGAGGATGACAT 600
TCGGAATCTTCACGTTACCGCTCAAGCC 629

FIGURE 4I

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Thermotoga maritima β -glucuronidase

ATGGTAAGACCGCAACGAAACAAGAAGAGATTTATTCTTATCTTGAATGG 50
AGTTTGAATCTTGAAGTAACCAGCAAAGACAGACCAATCGCCGTTCTG 100
GAAGCTGGAATGAGCAGTACCAGGATCTGTGCTACGAAGAAGGACCCTTC 150
ACCTACAAAACACCTTCTACGTTCCGAAGNACTTTCACAAAACACAT 200
CAGACTTTACTTTGCTGCGGTGAACACGGACTGCGAGGTCTTCCTCAACG 250
GAGAGAAAGTGGGAGAGAATCACATTGAATACCTTCCCTTCGAAGTAGAT 300
GTGACGGGGAAAGTGAAATCCGGAGAGAACTCAAGGTGAGGTGTTGTTGA 350
GAACAGATTGAAAGTGGGAGGATTTCCCTCGAAGGTTCAGACAGCGGCA 400
CTCACACCGTGGGATTTTTTGAAGTTTTCCACCTGCAAACTTCGACTTC 450
TTCCCCTACGGTGAATCATAAGGCCTGTTCTGATAGAGTTCACAGACCA 500
CGCGAGGATACTCGACATCTGGGTGGACACGAGTGAGTCTGAACCGGAGA 550
AGAAACTTGGAAGTGAAGTGAAGATAGAAGTCTCAGAAGAAGCGGTG 600
GGACAGGAGATGACGATCAAACCTTGGAGAGGAAGAGAAAAAGATTAGAAC 650
ATCCAACAGATTCGTGGAAGGGGAGTTCATCCTCGAAAACGCCAGGTTCT 700
GGAGCCTCGAAGATCCATATCTTTATCCTCTCAAGGTGGAACCTTGAAAAA 750
GACGAGTACACTCTGGACATCGGAATCAGAACGATCAGCTGGGACGAGAA 800
GAGGCTCTATCTGAACGGGAAACCTGTCTTTTGAAGGGCTTTGGAAAGC 850
ACGAGGAATCCCCGTTCTGGGGCAGGGCACCTTTTATCCATTGATGATA 900
AAAGACTTCAACCTTCTGAAGTGGATCAACGCGAATTCTTTCAGGACCTC 950
TCACTATCCTTACAGTGAAGAGTGGCTGGATCTTGCCGACAGACTCGGAA 1000
TCCTTGTGATAGACGAAGCCCCGCACGTTGGTATCACAAGGTACCACTAC 1050
AATCCCGAGACTCAGAAGATAGCAGAAGACAACATAAGAAGAATGATCGA 1100
CAGACACAAGAACCATCCCAGTGTGATCATGTGGAGTGTGGCGAACGAAC 1150
CAGAGTCCAACCATCCAGACGCGGAGGGTTTCTTCAAAGCCCTTTATGAG 1200

FIGURE 4J

09/936759

ACTGCCAATGAAATGGATCGAACACGCCCCGTTGTCATGGTGAGCATGAT 1250
GGACGCACCAGACGAGAGAACAAGAGACGTGGCGCTGAAGTACTTCGACA 1300
TCGTCTGTGTGAACAGGTACTACGGCTGGTACATCTATCAGGGAAGGATA 1350
GAAGAAGGACTTCAAGCTCTGGAAAAAGACATAGAAGAGCTCTATGCAAG 1400
GCACAGAAAGCCCATCTTTGTACACAGAATTCGGTGCGGACGCGATAGCTG 1450
GCATCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAG 1500
CTCGTTGAAAAGACGATCAGGCTCCTTTTGAAAAAAGACTACATCATCGG 1550
AACACACGTGTGGGCCTTTGCAGATTTTAAGACTCCTCAGAATGTGAGAA 1600
GACCCATTCTCAACCACAAGGGTGTTTTTACAAGAGACAGACAACCCAAA 1650
CTCGTTGCTCATGTACTGAGAAGACTGTGGAGTGAGGTT 1689

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BGUS -----MLYPINTETRGVFDLNGVWNFKLDYG----KGLEEKWYESKLTD---ISMAVP 47
 HGUS LGLQGGMLYPQESPSRECKELDGLWSFRADFSNRRRGFEEQWYRRPLWESGPTVDMVPV 60
 EGUS -----MLRPVETPTREIKKLDGLWAFSLDREN---CGIDQRWWESALQESR---AIAVP 48

BGUS SSYNDIGVTKEIRNHIGYVWYEREFTVPAYLKD---QRIVLRFGSATHKAIYVYNGELVV 104
 HGUS SSFNDISQDWRLRHFGVWVYEREVILPERWTQDLRTRVVLRIKSAHSYAIYVWVNGVDTL 120
 EGUS GSFNDQFADADIRNYAGNVWYQREVFIPKGWAG---QRIVLRFDAVTHYGVWVNNQEV 105

BGUS EHKGGFLPFEEAEINNSLRDG---MNRVTVAVDNILDSTLPVG-LYSERHEEGLGKVIR 159
 HGUS EHEGGYLPFEADISNLVQVGPLPSRLRITIAINNTLTPTTLPPGTIQYLTDTSKYPKGYF 180
 EGUS EHQQGYTPFEADVTPYVIAG---KSVRITVCVNELNWQTIPG---MVIDENGKKK--- 157

BGUS -NKPNDFFNYAGLHRPVKIYTTPTTYVEDISVVTDENGPT--GTVTYTVDFQG-KAETV 215
 HGUS VQNTYDFDFNYAGLQRSVLLYTTPTTYIDDITVTTTSVEQDS--GLVNYQISVKGSNLFLK 238
 EGUS -QSYFHDFFNYAGIHRVSMYLYTTPTNTWVDDITVVTHTVAQDCNHASVDWQVANG----DV 212

BGUS KVSVDDEEGKVASTEGLSGNVEIPNVILWEP-----LNTYLYQIKVELVNDGLT---ID 267
 HGUS EVRLDAENKVVANGTGTQGGQLKVPVSLWVYPMHERPAYLYSLEVQLTAQTSLGVPVSD 298
 EGUS SVELRDADQQVVATGQGTSGTLQVNVPHLWQP-----GEGYLYELCVTAKSQTEC----D 263

BGUS VYEEFPGVRTVEVNDGKFLINNKPFFYKGFKGKHEDTPINGRGFNEASNVMDFNILKWIGA 327
 HGUS FYTLFVGI RTVAVTKSQFLINGKPFYFHGVNKHEDADIRGKGFDPVLLVKDFNLLRWLGA 358
 EGUS IYPLRVGIRSVAVKGEQFLINHKKPFYFTGFRHEDADLRGKGFDPVLMVHDHALMDWIGA 323

BGUS NSFRTAHYPYSEELMRLADREGLVVIDETPAVGVLNFMATTGLGEGSERVSTWEKIR-- 385
 HGUS NAFRTSHYPYAEVVMQCDRYGIVVIDECPGVGLAL-----P-----QFFNNV 401
 EGUS NSYRTSHYPYAEMLDWADEHGI VVIDETAAVGFNLSLGIGFEAGNKPKEYSEEAVNGE 383

BGUS TFEHQDVLRELVS RDKNHPSVVMWSIANEAATEEGAYEYFKPLVELTKELDPQKRPVT 445
 HGUS SLHHMQVMEEVVRDKNHPAVVMWSVANEPASHLESAGYYLKMVIAHTKS LDPS-RPVT 460
 EGUS TQQAHLQAIKELIARDKNHPSVVMWSIANEPDTRPQGAREYFAPLAEATRKLDPTRPIT 442

BGUS IVLVFMATPETDKVAELIDVIALNRYNGWYFDGGDLEAAKVHLRQEFHAWNKRCPGKPI 505
 HGUS FVS--NSNYAADKGAPYVDVICLSYYSWYHDYGHLELIQLQLATQFENWYKKYQ-KPII 517
 EGUS CVNVMFCDAHTDTISDLFDVLCNRYYGWYVQSGDLETAEKVLEKELLAWQEKHL-QPII 501

BGUS ITEYGADTVAGFHDIDPVMFTEEYQVEYYQANHVVFD--EFENFVGEQAWNFAFATSQ 563
 HGUS QSEYGAETIAGFHQDPPLMFTEEYQKSLLQYHLGLDQKRRKYVVGELIWNFAFMTEQS 577
 EGUS ITEYGVDTLAGLHSMYTDMMWSEEYQCAWLDMYHRVFD--RVSAVVGEQVWNFAFATSQ 559

BGUS VMRVQGNKKGVFTRDRKPKLAHVFRERWTNIPDFGYKN----- 602
 HGUS PTRVLGNKKGIFTRQRPKSAAFLLRERYWKIAN-ET----- 613
 EGUS ILRVGGNKKGIFTRDRKPKSAAFLLQKRWGTGMNFGKPKQGGKQ 603

Staphylococcus :	DFGYKN----- :	607
Staph_homi :	DFGYQNASHDDI :	376
Staph_varn :	----- :	-
Thermotoga :	----- :	-
Enb/Salmon :	----- :	-
E_coli :	FGEXPOOGGKO :	603

[illegible]

Secretion of GUS_{Stp} in *E. coli*

WO 00/55333

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09936759
Title: MICROBIAL B-701
GLUCURONIDASE GENES, GENE
PRODUCTS AND USES THEREOF
Inventor(s): JEFFERSON ET AL.
DOCKET NO.: 076518-0150

09/936759

Cellular fractions were
assayed for glucuronidase and
galactosidase activity

Secretion Index was
calculated as follows:

- percent of total activity in the
periplasm fraction for
glucuronidase and
galactosidase was calculated
- galactosidase value was
subtracted from
glucuronidase as
"contamination"

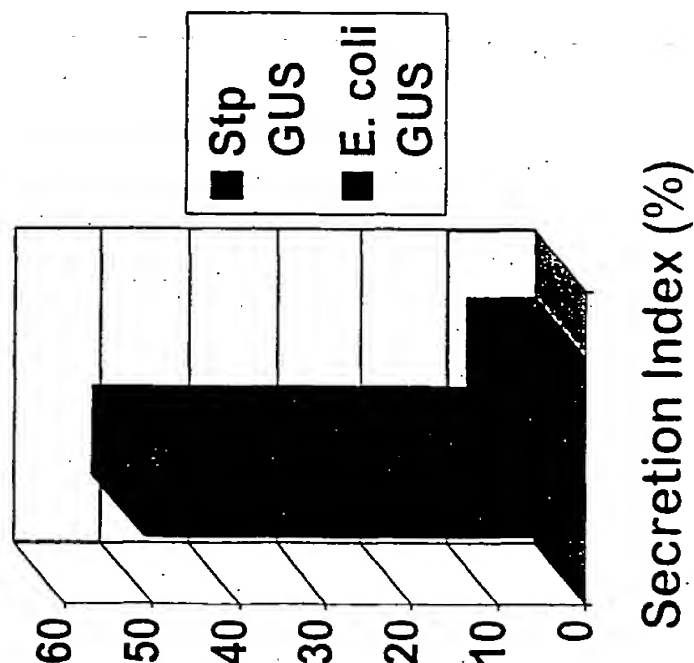


FIG. 6

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Thermal stability of β -glucuronidases

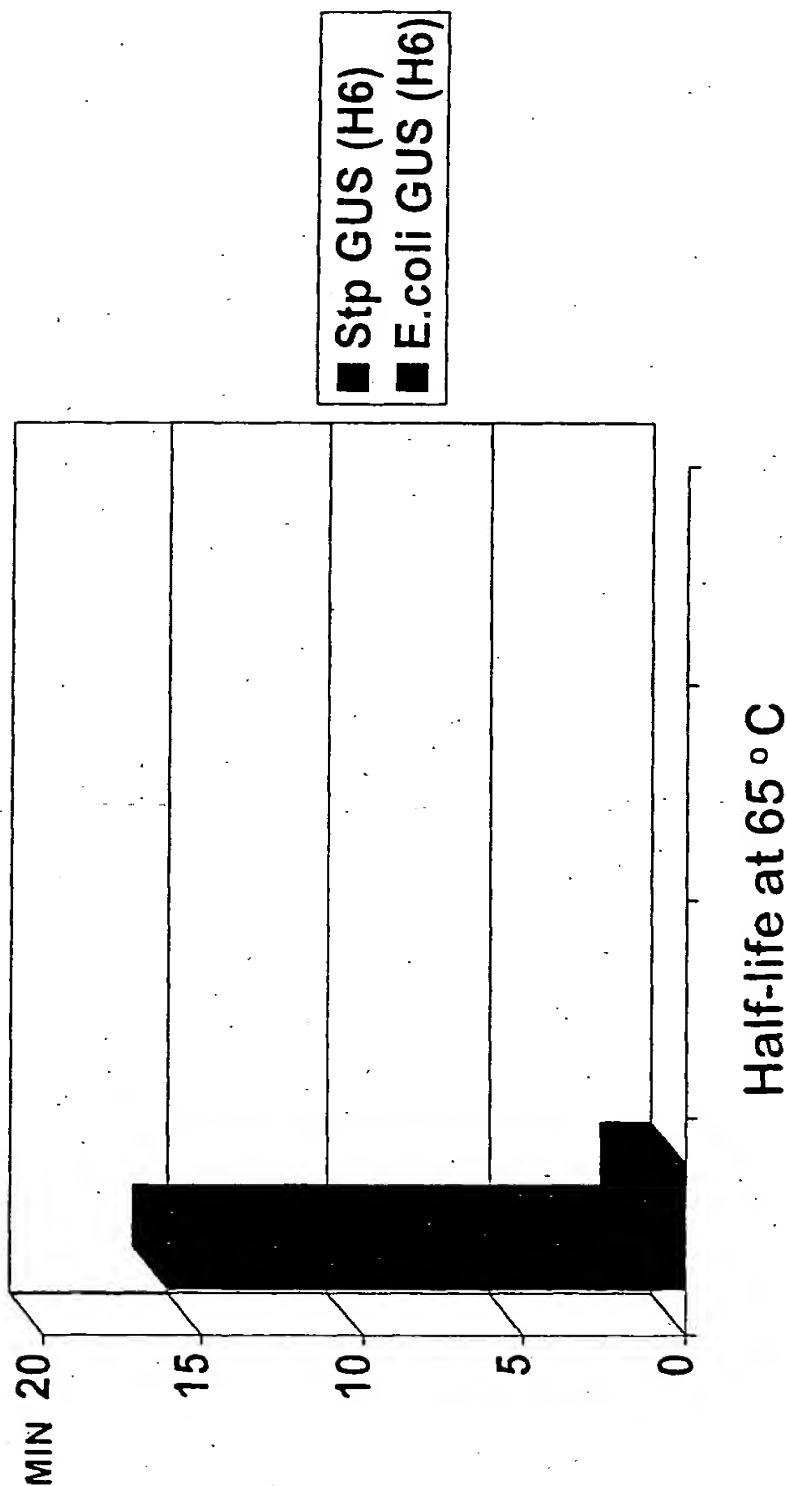
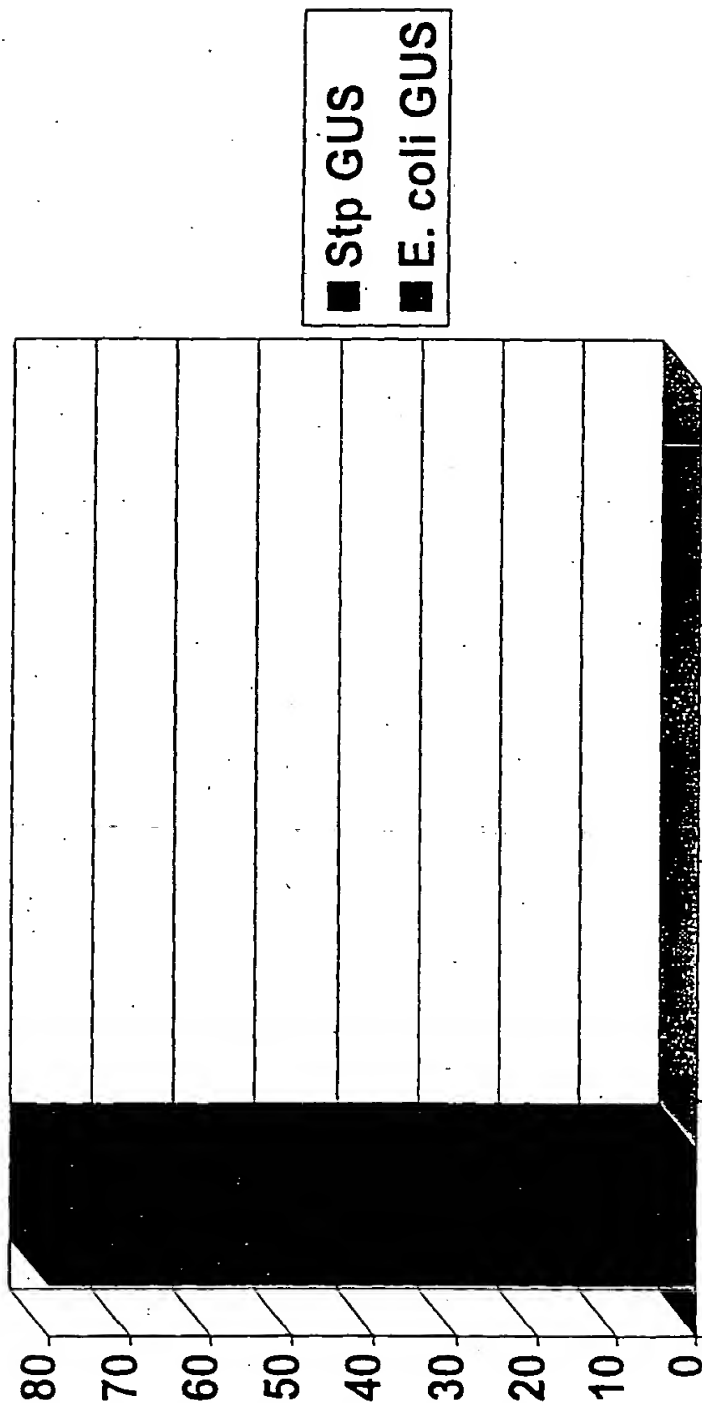


FIG. 7

Turnover number (37°C)

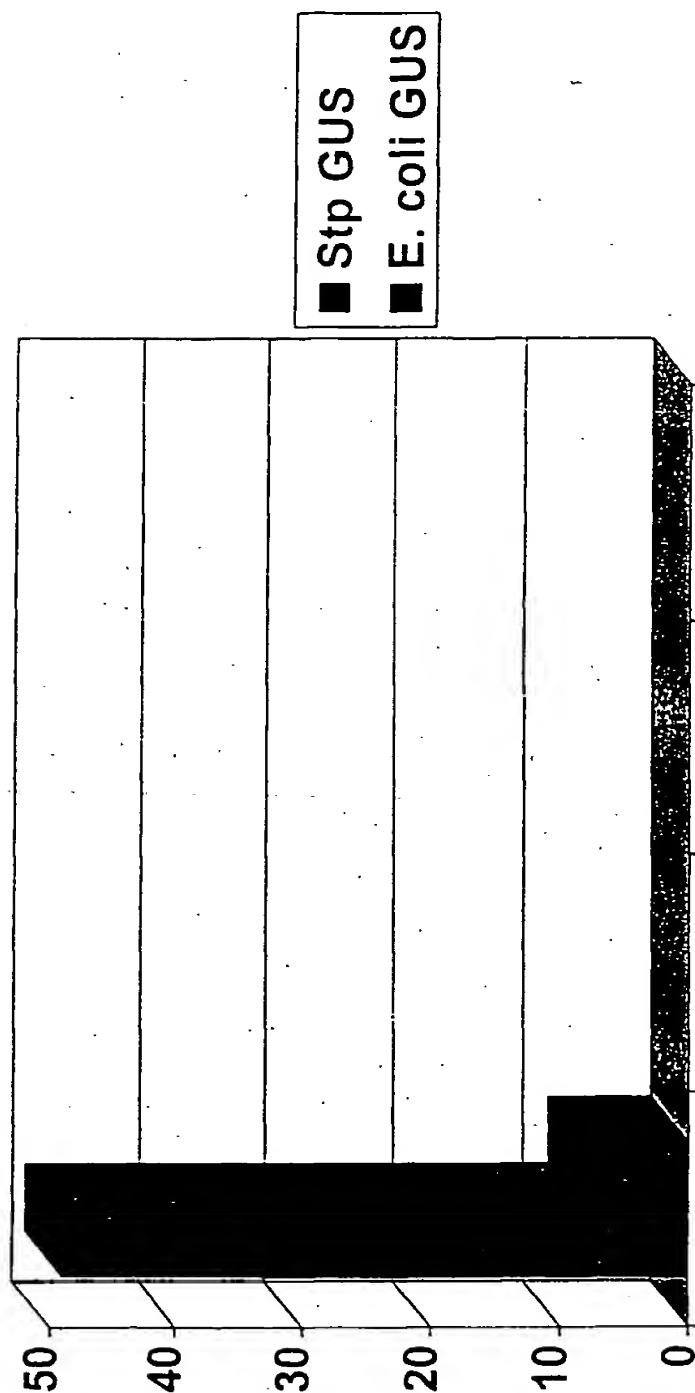


Nanomoles of p-nitrophenyl-glucuronide converted to p-nitrophenyl
per minute per μg of purified protein

9/936759

FIG. 8

Turnover number (RT)



Nanomoles of p-nitrophenyl-glucuronide converted to p-nitrophenyl
per minute per μg of purified protein

FIG. 9

WO 00/55333

Title: MICROBIAL B
GLUCURONIDASE GENES, GENE
PRODUCTS AND USES THEREOF
Inventor(s): JEFFERSON ET AL.
DOCKET NO.: 076518-0150

PCT/US00/07107

09936759 09/936754

09/936759

Effect of detergents on GUS^{stp} activity

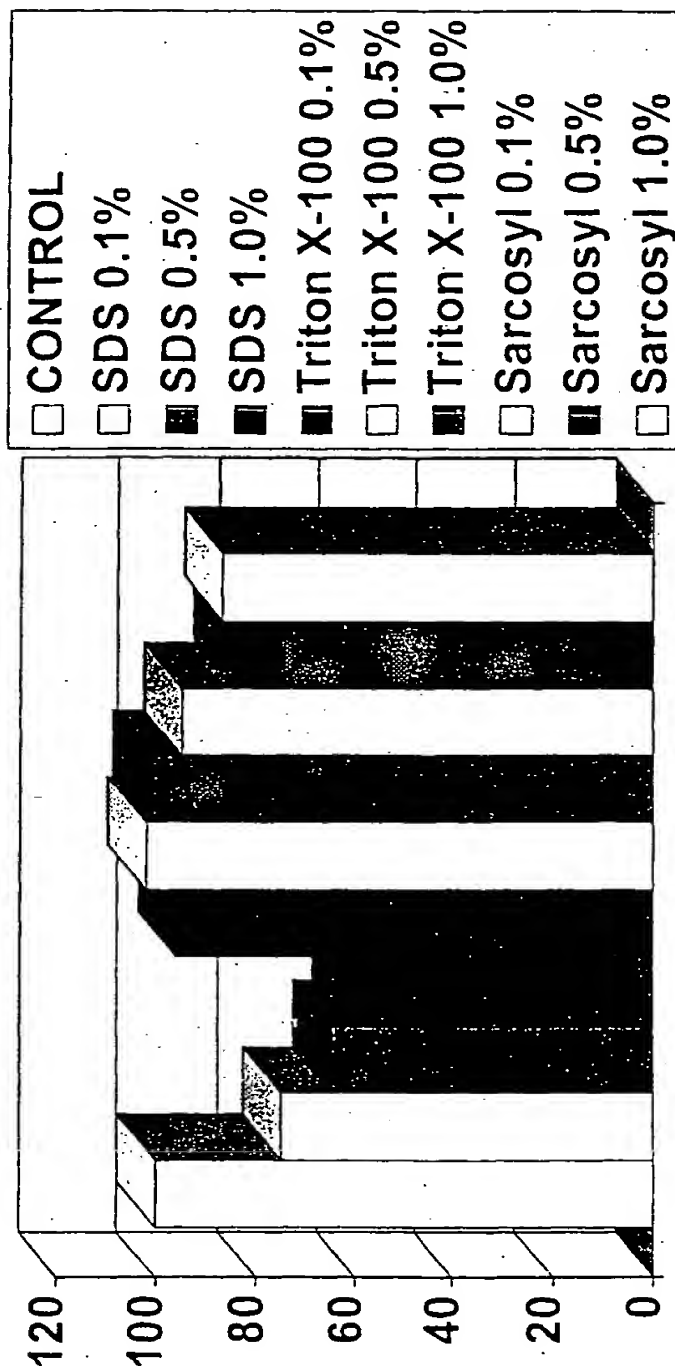


FIG. 10

Effect of glucuronic acid, the reaction product, on GUS^{stp} activity

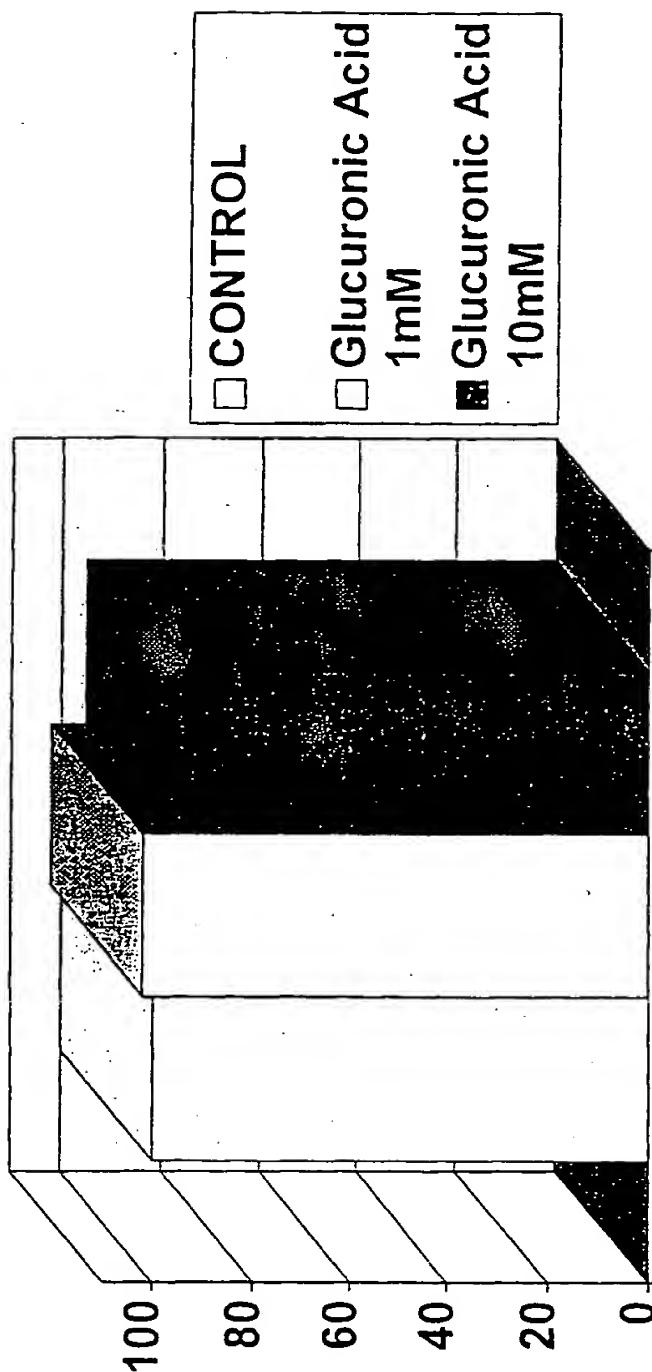


FIG. 11

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GUS^{stp} activity in salt and in different organic solvents

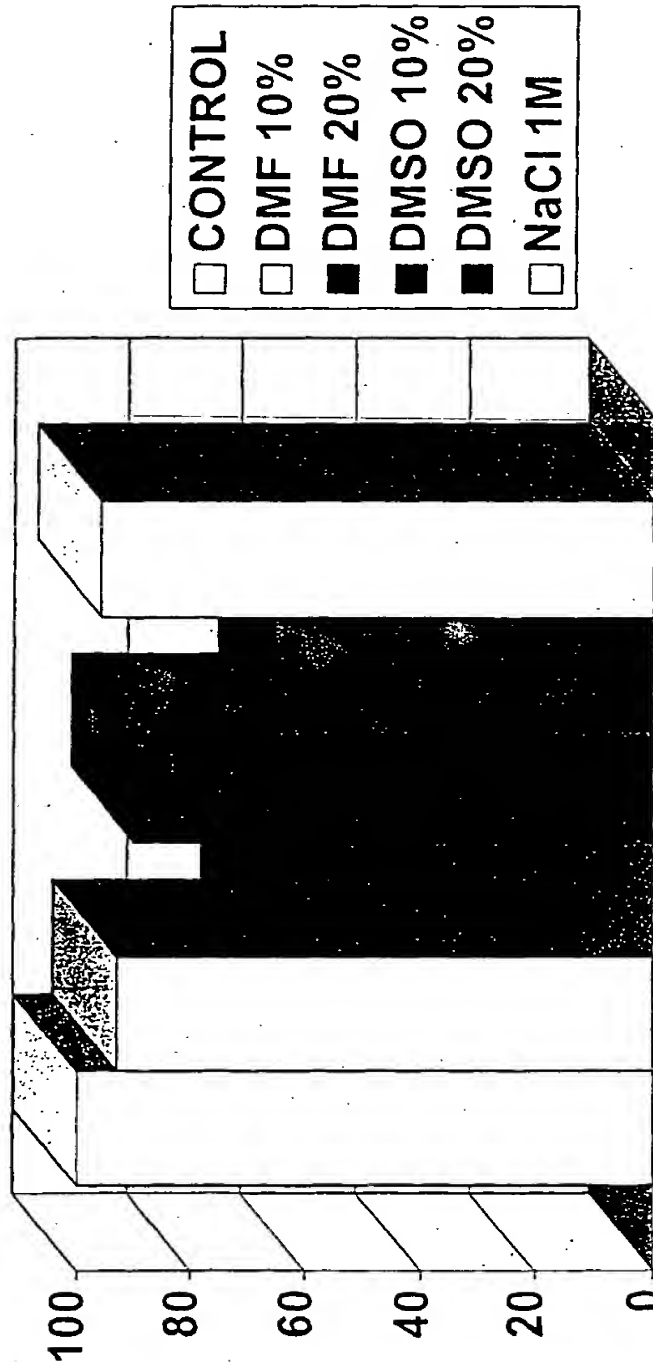


FIG. 12

FIGURE 13A

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MetValAspLeuThrSerLeuTyr
ATACGACTCA CTAGTGGGTC GACCCATGGTAGATCTGACTAGTCTGTAC
Sali NcoI BglII

ProIleAsnThrGluThrArgGlyValPheAspLeuAsnGlyValTrpAsn
CCGATCAACACCGAGACCCGTCGCGTCTTCGACCTCAATGGCGTCTGGAAC

PheLysLeuAspTyrGlyLysGlyLeuGluGluLysTrpTyrGluSerLys
TTCAAGCTGGACTACGGGAAAGGACTGGAAGAGAAGTGGTACGAAAGCAA

LeuThrAspThrIleSerMetAlaValProSerSerTyrAsnAspIle
GCTGACCGACACTATTAGTATGGCCGTCCCAAGCAGTTACAATGACATTG

GlyValThrLysGluIleArgAsnHisIleGlyTyrValTrpTyrGluArg
GCGTGACCAAGGAAATCCGCAACCATATCGGATATGTCTGGTACGAACGT

GluPheThrValProAlaTyrLeuLysAspGlnArgIleValLeuArgPhe
GAGTTCACGG TGCCGGCCTATCTGAAGGATCAGCGTATCGTGCTCCGCTT

GlySerAlaThrHisLysAlaIleValTyrValAsnGlyGluLeuVal
CGGCTCTGCAACTCACAAAGCAATTGTCTATGTCAATGGTGAGCTGGTCG

ValGluHisLysGlyGlyPheLeuProPheGluAlaGluIleAsnAsnSer
TGGAGCACAAGGGCGGATTCTCTGCCATTCTGAAGCGGAAATCAACAACCTCG

LeuArgAspGlyMetAsnArgValThrValAlaValAspAsnIleLeuAsp
CTGCGTGATGGCATGAATCGCGTCACCGTCGCCGTGGACAACATCCTCGA

AspSerThrLeuProValGlyLeuTyrSerGluArgHisGluGluGly
CGATAGCACCTCCCGGTGGGGCTGTACAGCGAGCGCCACGAAGAGGGCC

LeuGlyLysValIleArgAsnLysProAsnPheAspPhePheAsnTyrAla
TCGGAAAAGTCATTCTGTAACAAGCCGAACCTTCGACTTCTTCAACTATGCA

GlyLeuHisArgProValLysIleTyrThrThrProPheThrTyrValGlu
GGCCTGCACCGTCCGGTGAAAATCTACACGACCCCGTTTACGTACGTCTGA

AspIleSerValValThrAspPheAsnGlyProThrGlyThrValThr
GGACATCTCGGTTGTGACCGACTTCAATGGCCCAACCGGGACTGTGACCT

TyrThrValAspPheGlnGlyLysAlaGluThrValLysValSerValVal
ATACGGTGGACTTTCAAGGCAAAGCCGAGACCGTGAAAGTGTCGGTCTGTG

AspGluGluGlyLysValValAlaSerThrGluGlyLeuSerGlyAsnVal
GATGAGGAAGGCAAAGTGGTCGCAAGCACCGAGGGCCTGAGCGGTAACGT

GluIleProAsnValIleLeuTrpGluProLeuAsnThrTyrLeuTyr
GGAGATTCCGAATGTCATCCTCTGGGAACCACTGAACACGTATCTCTACC

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FIGURE 13B

GlnIleLysValGluLeuValAsnAspGlyLeuThrIleAspValTyrGlu
CAGATCAAAGTGGAAGTGGTGAACGACGGACTGACCATCGATGTCTATGAA

GluProPheGlyValArgThrValGluValAsnAspGlyLysPheLeuIle
GAGCCGTTCCGGCGTGCGGACCGTGGAAGTCAACGACGGCAAGTTCCTCAT

AsnAsnLysProPheTyrPheLysGlyPheGlyLysHisGluAspThr
CAACAACAAACCGTTCTACTTCAAGGGCTTTGGCAAACATGAGGACACTC

ProIleAsnGlyArgGlyPheAsnGluAlaSerAsnValMetAspPheAsn
CTATCAACGGCCGTGGCTTTAACGAAGCGAGCAATGTGATGGATTTCAAT

IleLeuLysTrpIleGlyAlaAsnSerPheArgThrAlaHisTyrProTyr
ATCCTCAAATGGATCGGCGCCAACAGCTTCCGGACCGCACACTATCCGTA

SerGluGluLeuMetArgLeuAlaAspArgGluGlyLeuValValIle
CTCTGAAGAGTTGATGCGTCTTGCGGATCGCGAGGGTCTGGTCTGTGATCG

AspGluThrProAlaValGlyValHisLeuAsnPheMetAlaThrThrGly
ACGAGACTCCGGCAGTTGGCGTGACCTCAACTTCATGGCCACCACGGGA

LeuGlyGluGlySerGluArgValSerThrTrpGluLysIleArgThrPhe
CTCGGCGAAGGCAGCGAGCGCGTCAGTACCTGGGAGAAGATTCCGACGTT

GluHisHisGlnAspValLeuArgGluLeuValSerArgAspLysAsn
TGAGCACCATCAAGACGTTCTCCGTGAAGTGGTGTCTCGTGACAAGAACC

HisProSerValValMetTrpSerIleAlaAsnGluAlaAlaThrGluGlu
ATCCAAGCGTCGTGATGTGGAGCATCGCCAACGAGGCGGCGACTGAGGAA

GluGlyAlaTyrGluTyrPheLysProLeuValGluLeuThrLysGluLeu
GAGGGCGCGTACGAGTACTTCAAGCCGTTGGTGGAGCTGACCAAGGAACT

AspProGlnLysArgProValThrIleValLeuPheValMetAlaThr
CGACCCACAGAAGCGTCCGGTCACGATCGTGCTGTTTGTGATGGCTACCC

ProGluThrAspLysValAlaGluLeuIleAspValIleAlaLeuAsnArg
CGGAGACGGACAAAGTCGCCGAAGTGAATGACGTCATCGCGCTCAATCGC

TyrAsnGlyTrpTyrPheAspGlyGlyAspLeuGluAlaAlaLysValHis
TATAACGGATGGTACTTTCGATGGCGGTGATCTCGAAGCGGCCAAAGTCCA

LeuArgGlnGluPheHisAlaTrpAsnLysArgCysProGlyLysPro
TCTCCGCCAGGAATTTACGCGTGGAACAAGCGTTGCCAGGAAAGCCGA

IleMetIleThrGluTyrGlyAlaAspThrValAlaGlyPheHisAspIle
TCATGATCACTGAGTACGGCGCAGACACCGTTGCGGGCTTTACGACATT

AspProValMetPheThrGluGluTyrGlnValGluTyrTyrGlnAlaAsn
GATCCAGTGATGTTACCGAGGAATATCAAGTCGAGTACTACCAGGCGAA

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FIGURE 13C

HisValValPheAspGluPheGluAsnPheValGlyGluGlnAlaTrp
CCACGTCGTGTTTCGATGAGTTTGAGAACTTCGTGGGTGAGCAAGCGTGGA

AsnPheAlaAspPheAlaThrSerGlnGlyValMetArgValGlnGlyAsn
ACTTCGCGGACTTCGCGACCTCTCAGGGCGTGATGCGCGTCCAAGGAAAC

LysLysGlyValPheThrArgAspArgLysProLysLeuAlaAlaHisVal
AAGAAGGGCGTGTTCACTCGTGACCGCAAGCCGAAGCTCGCCGCGCACGT

PheArgGluArgTrpThrAsnIleProAspPheGlyTyrLysAsn
CTTTCGCGAGCGCTGGACCAACATTCCAGATTTTCGGCTACAAGAACGCTA

SerHisHisHisHisHisHisVal *
GCCATCACCATCACCATCACGTGTGAATTGGTGACCG
NheI PmlI BstEII

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FIGURE 14

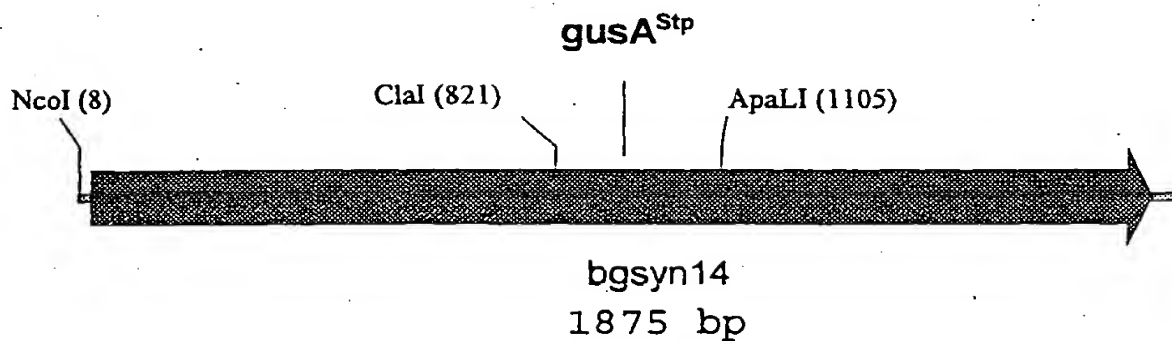
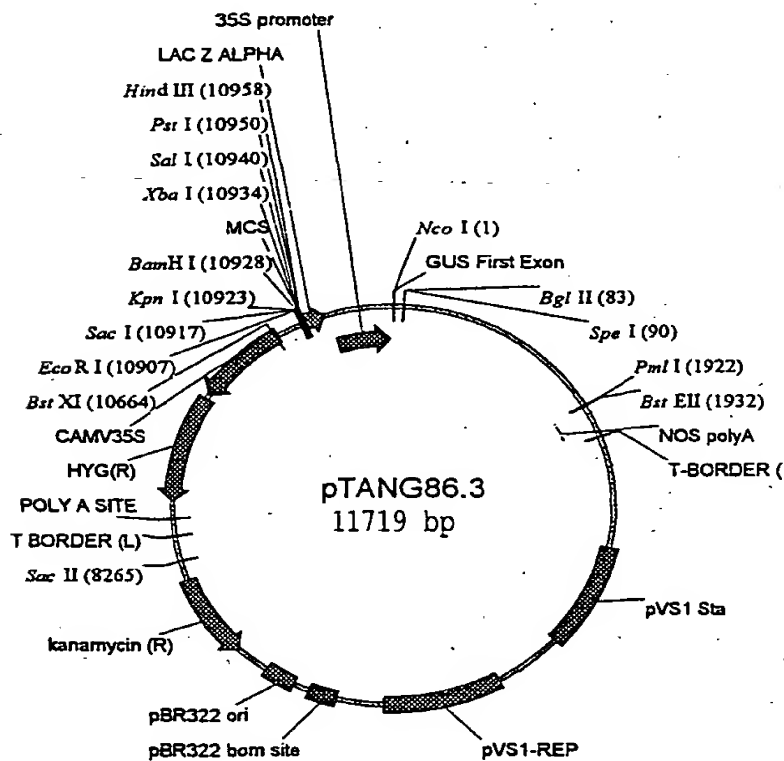
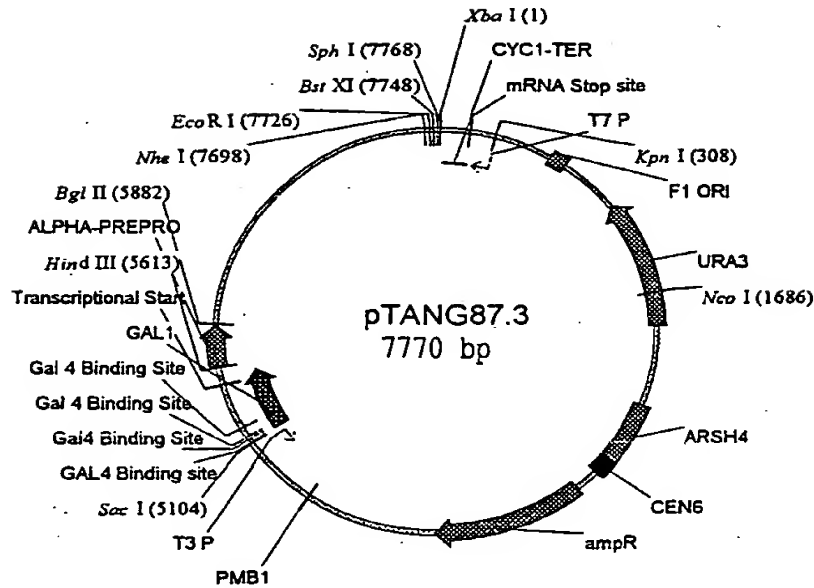


FIGURE 15

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FIGURE 16

```
1  ATGTTACGTT CTGTGCGAAAC CGCGACGCGA GAAATCAAAA AACTGGACGG
51  CCTGTGGTCG TTTTGTATGG ATAGCGAAGA GTGCGGCAAC GCGCAGCAAT
101 GGTGGCGTCA ACCGTTACCC CAAAGCCGCG CTATCGCCGT TCCGGGAAGC
151 TATAACGATC AGTTTGCCGC TGCCGAGATC CGCAATTATG TTGGCAACGT
201 CTGGTATCAG CGTGAGATAC GCATCCCGAA AGGCTGGGAT CGCCAGCGCA
251 TAGTGCTGCG CTTTGATGCG GTGACTCACT ATGGAAAAGT TTGGGTCAAT
301 GACCAATTTT TAATGGAACA TCAGGGCGGC TACACGCCGT TTGAAGCGGA
351 TATCAGCCAC CTTATCTCCG CCGGGGAATC CGTGCGTATC ACGGTATGCG
401 TGAATAACGA GCTGAACTGG CAGACGATCC CGCCGGGCGT TGTGACCCAG
451 GGCCTAAACG GTAAGAAGCA GCAAGCGTAT TTCCATGATT TCTTTAACTA
501 CGCCGGTATT CATCGCAGCG TAATGCTGTA CACCACGCCG AAAACTTTTG
551 TGGAAGATAT TACCGTCGTG ACGCAGGTTG CTGACGATCT GGCTCAGGCT
601 ACCGTCGCCT GGCAGGTACG GCGGAATGGC GAAGTGCGTG TAGAGCTACG
651 TGACGCGGAG CAACAGCTTG TCGCTTCGGG GCAAGGGGAA AAAGGTGAAC
701 TGCTGCTGGA AGGGCCGCGG CTGTGCGAGC CTGGCGAGGG CTATCTTTAT
751 GAACTGCGGG TCATCGCGCA GCATCAGGAC GAGCAGGATG AATATCCGCT
801 GCGCGTCGGT ATTCGCTCGG TAGAAGTAAA AGGGGAGCAG TTCCTGATCA
851 ACCATAAGCC TTTCTATTTT ACCGGGTTCT GACGTCATGA AGATGCCGAT
901 CTGCGCGGTA AGGGTTTTGA TAACGTGCTG ATGGTGCACG ACCACGCGCT
951 AATGGACTGG ATCGGTGCGA ACTCTTACCG TACCTCGCAT TACCCTTATG
1001 CCGAAGAGAT GCTCGACTGG GCGGACGAAC ATGGCATCGT CATCATTGAT
1051 GAAACGGCCG CCGTCGGATT CAACCTGTCT TTAGGGATTA GCTTTGATGT
1101 CGGCGAAAAA CCCAAAGAGC TCTACAGCGA TGAGGCCGTG AACGATGAAA
1151 GCGAGCGCGC GCACCTGCAG GCAATTAAGG AGCTGATTGC CCGCGATAAG
1201 AACCACCCAA GCGTCGTGAT GTGGAGTATC GCCAACGAAC CGGATACCCG
1251 CCCGAACGGC GCGCGCGAAT ACTTCGCTCC GCTGGCGCAG GCAACGCGCG
1301 AACTCGATCC TACACGTCCG ATAACCTGCG TGAACGTGAT GTTCTGCGAT
1351 GCGGAAAGCG ACACCATTAC CGATCTCTTT GATGTCGTTT GCCTGAACCG
1401 CTACTACGGC TGGTATGTAC AAAGCGGCGA TCTGGAGAAG GCTGAGAAAG
1451 TGCTGGAGAA AGAGCTTCTG GCCTGGCAGG AGAAACTCCA CCGCCCGATT
1501 ATCATCACCG AATACGGCGT CGATACGCTT GCAGGCCTGC ATTCCATGTA
1551 CAACGATATG TGGAGCGAAG AGTACCACTG CGCCTGGCTT GATATGTACC
1601 ATCGCGTGTT TGATCGCGTC AGCGCCGTCG TCGGCGAGCA GGTATGGAAC
1651 TTCGCCGACT TCGCCACTTC GCAGGGCATT ATGCGCGTTG GCGGCAACAA
1701 AAAAGGTATA TTCACCCGCG ACAGAAAACC AAAATCGGCG GCCTTCCTGC
1751 TGCAAAAACG CTGGACCGGC ATGGACTTTG GCGTGAAGCC CCAGCAGGGA
1801 GATAAATAAT GA
```

FIGURE 17

1 MLRSVETATR EIKKLDGLWS FCMDSEECGN AQQWWRQPLP QSRAIAVPGS
51 YNDQFAAAEI RNYVGNVWYQ REIRIPKGWD RQRIVLRFDA VTHYGKVVWN
101 DQFLMEHQGG YTPFEADISH LISAGESVRI TVCVNNELNW QTIPPGVVTO
151 GVNGKKQQAY FHDFPNYAGI HRSVMLYTTT KTFVEDITVV TQVADDLAQA
201 TVAWQVRANG EVRVELRDAE QQLVASGQGE KGELLLEGPR LWQPGEGYLY
251 ELRVIAQHQD EQDEYPLRVG IRSVEVKGEQ FLINHKPFYF TGFRGHEDAD
301 LRGKGFNDVL MVHDHALMDW IGANSYRTSH YPYAEEMLDW ADEHGIVIID
351 ETAAVGFNLS LGISFDVGEK PKELYSDEAV NDETQRAHLQ AIKELIARDK
401 NHPSVVMWSI ANEPDTRPNG AREYFAPLAQ ATRELDPTRP ITCVNMFCF
451 AESDTITDLF DVVCLNRYYG WYVQSGDLEK AEKVLEKELL AWQEKLHRPI
501 IITEYGVDTL AGLHSMYNDM WSEEQCAWL DMYHRVFDRV SAVVGEQVWN
551 FADFATSQGI MRVGGNKKGI FTRDRKPKSA AFLQKRWTG MDFGVKPPQG
601 DK

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Staph	:	MVDLTSLYEINTETRGVFDLNGVNHKTFYG-KGLE	:	35
E coli	:	-----MLREVEITPTRETKKLDGLHAFSTDERENGCID	:	31
Sal	:	-----MLRSVETATRETKKLDGLHSECMDSSECCNA	:	31

Staph	:	EKVYESKLTDTTISMAVESSYNDIGVTKEIRNHIGYV	:	71
E coli	:	QRWVESALQESRAIAVEGSEFNDQFADADIRNYAGNV	:	67
Sal	:	QQWWRQPLPOSRAIAVEGSEYNDQFAAAEIRNYVGNV	:	67

Staph	:	WYEREFVTPAYLKDQRIVLRFSGATHKAIYVNGEL	:	107
E coli	:	WYOREVFPKGWAGQRIVLRFDAVTHYGVVWVNNCE	:	103
Sal	:	WYOREIRFPKGDQRIVLRFDAVTHYGVVWVNDQF	:	103

Staph	:	VVEHKGGFLPFEAEINNSLRDGMN-RVTVAVDNILD	:	142
E coli	:	VMEHQGGYTPFEADVTPYVIAGKSVRLITVCVNNELN	:	139
Sal	:	IMEHQGGYTPFEADISHLISAGESVRLITVCVNNELN	:	139

Staph	:	DSTLEFVGLYSERHEEGLGKVIRNKPNDFFNYAGLE	:	178
E coli	:	WQTHPECMVITDEN---GKKKCS-YFHDFFNYAGLEH	:	171
Sal	:	WQTHPEGVVITQGVN---GKKQCA-YFHDFFNYAGLEH	:	171

Staph	:	RPVKIYTTFFTYVEDISVVTOFNGPTGTVTYTVDFQ	:	214
E coli	:	RSVMLYTTENTWVDDITVVVTHVAOCNHASVDWQVV	:	207
Sal	:	RSVMLYTTFKTFVEDITVVVTOVADDLAQATVAWQVR	:	207

Staph	:	GKAETVKVSVVDEEGKVASTEGLSGNVEIPNVILW	:	250
E coli	:	ANGD-VSVELRDADQQVATGCGTSGTLQVVNEHLW	:	242
Sal	:	ANGE-VRVELRDADQQQLVASGCGEKCELLLEGERLW	:	242

Staph	:	EPLNTYLYQIKVELVNDGLTIDVVEEPFGVRTVEVN	:	286
E coli	:	QPGEGLYVELCVTAKSO-TECDIYPLRVGERSVAVK	:	277
Sal	:	QPGEGLYVELRVIAQHO-DEODEYPLRVGERSVEVK	:	277

FIG. 18A

Staph : DGKFLINNKPFYFKCFCKHEDTPIINCRGFNEASNVV : 313
 E coli : GEQFLINHKPFYFTGSGRHEDADLRCKGFDNVLMVH : 313
 Sal : GEQFLINHKPFYFTGSGRHEDADLRCKGFDNVLMVH : 313

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Staph : DFNILKWIIGANSFRTAHYPVSEELMRIADREGLVVI : 358
 E coli : DHALMDWIGANSYRTSHYPVAAEEMLDWADEHGHVVI : 349
 Sal : DHALMDWIGANSYRTSHYPVAAEEMLDWADEHGHVVI : 349

Staph : DETPAVGCVHINFMATTGLGEGSERVSTWEKIR--TF : 392
 E coli : DETPAVGCFNLSLGIGFEAGNPKKELYSEAVNGETG : 385
 Sal : DETPAVGCFNLSLGISEFDVCEKPKELYSDAVNDETO : 385

Staph : EHFQDVLRELVS RDKNHPSVVMWSIANEAATEEBCA : 428
 E coli : QHFLQAIKELIARDKNHPSVVMWSIANEPDTRFQCA : 421
 Sal : RAHFLQAIKELIARDKNHPSVVMWSIANEPDTRFNGA : 421

Staph : YEYFKPLVELTKELDPOKRPVTIIVLFVMAPEHDKV : 464
 E coli : REYFAPLAETATRKLDP-TRPIITGVNVVMFCDAHEDTI : 456
 Sal : REYFAPLAQATRELDP-TRPIITGVNVVMFCDAESDII : 456

Staph : ABLIDVIALNRYNGWYFDGCDLEAAKVHLROEFHAW : 500
 E coli : SLEEDVLCNRYYGWYVQSGDLETAEKVLEKELLAW : 492
 Sal : TDEEDVVCNRYYGWYVQSGDLEKAQKVLEKELLAW : 492

Staph : NKRCPGKPIIMITEYGADIVAGEFDIDPVMFTEEYQV : 536
 E coli : QEKKEH-QPIIITEYGVDITLAGLHSMYNDMWSEYQC : 527
 Sal : QEKKEH-RPIIITEYGVDITLAGLHSMYNDMWSEYQC : 527

Staph : EYYQANHVVVFDEFENFVGEQAWNFAADFATSQGVMRV : 572
 E coli : AWEDMYHRVFDREVSAVVGEQAWNFAADFATSQGLRV : 563
 Sal : AWEDMYHRVFDREVSAVVGEQAWNFAADFATSQGLMRV : 563

FIG. 18B

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File: MICROBIAL 2-
09 GEUGURONIDASE GENE
PROPERTIES AND USES THEREOF
Inv(s): JEFFERSON ET AL.
DOCKET NO.: 076518-0150

Staph	:	QGNKKGVFTRDRKPKLAHVFRERWTNIPDFGYKN-	:	097936759
E coli	:	CGNKKGLEFTRDRKPKSA AFL LQKRWTCM-NFCERPC	:	598
Sal	:	CGNKKGLEFTRDRKPKSA AFL LQKRWTCM-DFGVKPO	:	598

Staph	:	-----	:	-
E coli	:	CGGRQ--	:	603
Sal	:	CGDRK---	:	602

FIG. 18C

Staph : -----ATGGTAGATCTGACTAGTCTGTACCC : 11
 E.coli : TTATTATCTTAATCAGCAGTCCCTTATGTTACGTCC : 36
 Sal : -----ATGCTIACGTC : 11

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Staph : GATCAACACCGAGACCCGTCGCGTCTTCGACCTCAA : 62
 E.coli : TGTAGAAACCCCAACCGCGTGAAATCAAAAAAAGTCCA : 72
 Sal : TGTGAAACCGCGAGCCGAGAAATCAAAAAAAGTCCA : 47

Staph : TGGCGTCTGGAACCTTCAAGCTGGACTACGGGAAA-- : 96
 E.coli : CCGCCCTGTGGGCAATTCAGTGTGGATCGCGAAAAGTCC : 108
 Sal : CCGCCCTGTGGTCTGTTTGTATGGATAGCGAAGAGTG : 83

Staph : -GGACTGGAAGAGAAAGTGGTACGAAAGCAAGCTGAC : 131
 E.coli : TGGAAATCATCAGCGTGTGGTGGAAAGCGCGCTTACA : 144
 Sal : CCGCAACCGCGCAGCAATGGTGGCGTCAACCGTTACC : 119

Staph : CGACACTATTAGTATGCGCGTCCCAAGCAGTTACAA : 167
 E.coli : AGAAAGCCGGGCAATTCCTGTGCCAGGCACCTTTTAA : 180
 Sal : CCAAGCCCGCTATCGCGGTCCGGAAGCTATAA : 155

Staph : TGACATTGGCGTGACCAAGGAAATCCGCAACCATAT : 203
 E.coli : CGATCAGTTCCCGATGCGAGATATTCGTAATTATGC : 216
 Sal : CGATCAGTTTCCCGGTGCGAGATCCGCAATTATGT : 191

Staph : CGGATAAGTCTGGTACGAACGTTGAGTTCACGGTGGC : 239
 E.coli : GGGCAACGTCTGGTATCAGCGCGAAGTCTTTATACC : 252
 Sal : TGGCAACCTCTGGTATCAGCGTGAGATACGATCCC : 227

Staph : GGCCTATCTCAAGGATCAGCGTATGGTGTCTCCGCTT : 275
 E.coli : GAAAGGTTGGCCAGCCAGCGTATCGTGTCTCGCTTT : 288
 Sal : GAAAGGCTGGGATCGCCAGCGCATAGTGCTGCGCTT : 263

FIG. 19A

Staph : CCGCTCTGCAACTCACAAGCAATTGTCTATCTCAA : 09/936759
E.coli : CGATGCCGTCACTCAATTACCGCAAGTGTGGGTCAA : 324
Sal : TGATGCCGTCACTCACTATGGAAAGTTTGGGTCAA : 299

Staph : TGGTGAGCTGGTCTGGAGCAACAGGGCGGATTCT : 347
E.coli : TAATCAGGAAGTGATGGAGCATCAGGGCGGCTATAC : 360
Sal : TEACCAATTTTAAATGGAAACATGAGCGCGGCTACAC : 335

Staph : GCCATTTCGAAGCGGAATCAACAATCGCTGCGTGA : 383
E.coli : GCCATTTCGAAGCGGATGTACCGGCGAATGTTATGCG : 396
Sal : CCGGTTTGAAGCGGATATCAGGGAGCTTATCTCCGC : 371

Staph : TGGCATCAAT---CGCGTCACCGTCCCGGTGGACAA : 416
E.coli : GCGGAAAAGTGTAAGTATCACCGTTTGTGTGAACAA : 432
Sal : CCGCGAATCCGTGCGTATCACCGTATGCGTGAAATA : 407

Staph : CATCTTCGACGATAGCACCCCTCCCGGTGGGGCTGTA : 452
E.coli : CGAATGAACTGGCAGACTATCCCCCGGGGAAT-CG : 467
Sal : CGAGCTGAAGTGGCAGACGATCCCCCGGGGCGT-TG : 442

Staph : CAGCGAGCGCCACGAAGAGGGCCTCCGAAAAGTCAT : 488
E.coli : TGATTACCGACGAAAACGG-----CAAGAAAAAGCAG : 499
Sal : TGACCCAGGGCGTAACGG-----TAAGAAAGCAGCAA : 474

Staph : TCGTAACAAGCCGAACCTCGACTTCTTCAACTATGC : 524
E.coli : TCTTACTT-----CGATGATTTCTTTAACTATGC : 528
Sal : GCGTATTT-----CGATGATTTCTTTAACTACGC : 503

Staph : AGGCCCTGCACCGTCCGCTGAAAATCTACACGACCCC : 560
E.coli : CCGCATCCATCGCAGCGTAATGGTGTACACCACGCC : 564
Sal : CCGTATTCATCGCAGCGTAATGCTGTACACCACGCC : 539

FIG. 19B

Staph : GTTACGTACGTCCAGGACATCTCGGTGTGACCGA : 596
 E.coli : GATCAGCTGGGTGGACGATATCACCGTGGTGACCGA : 600
 Sal : GAAACTTTTGTGGAAGATATTACCGTGGTGACCGA : 575

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Staph : CTTCAAATGGCCCAACCGGACTGTGACCTATAGCGT : 632
 E.coli : TGGCGGGCAA--GACTGTAAACCAACCGTGTGTGTGAG : 634
 Sal : GGTTCCTGAG--GATCTGCTCAGGGTAGCCTGGCCG : 609

Staph : GGACTTTCAAGCCAAAGCCGAGACCGTGAAAGTGTC : 668
 E.coli : TGGCAGGTGGTGGCCAAATGGTGAT-CTCAGCGTTGA : 669
 Sal : TGGCAGGTACGGCGCAATGGCCAA-GTCCGTGTAGA : 644

Staph : CGTCGTGATGAGCAAGGCAAGCTGGTGGCAAGCAC : 704
 E.coli : AGTGGGTGATGCGGATCAACAGGTGGTGGCAAGTGG : 705
 Sal : GGTACGTGACCGCGGAGCAACAGCTTGTGCTTGGGG : 680

Staph : CGAGGGCTGAGCGGTAACTGGCAGATTCCGAATGT : 740
 E.coli : ACAAAGGCACTAGCGGGACTTGGCAAGTGGTGTATCC : 741
 Sal : GCAAGGGGAAAAAGGTGAAGTGTGCTGCTGCAAGGGCC : 716

Staph : CATCCTCTGGGAAACCACTGAACACGTATCTGTACCA : 776
 E.coli : GCACCTCTGGGAACCGGGTGAAGGTATCTGTAT-- : 775
 Sal : GCGGCTGTGGGAGCCTGGCGAGGGCTATCTTTAT-- : 750

Staph : GATCAAAGTGAAGTGGTGAACGACGGACTGACCAT : 812
 E.coli : GAACGTGTGGTGCACAGCCAAAAGCCAGACAGAGTGT : 811
 Sal : GAACGTGGGGTGAATCGCGCAAGATCAGGACGAGCAG : 786

Staph : CGATGTCTATGAAGAGCCGTTCGGCGTGGCGACCGT : 848
 E.coli : -GATATCTACCGGCTTCGGGTGGCGATCCGGTCAGT : 846
 Sal : -GATGAATATCCGCTGCGGCTCGGTATTCGGTCCGT : 821

FIG. 19C

Staph	:	GGAAGTCAACGACGGCAAGTTCCTCATCAACAACAA	:	884
E.coli	:	GGCAGTCAACGGCGCAACAGTTCCTGATTAACGACAA	:	882
Sal	:	AGAAGTAAAAGGGCAGCAGTTCCTGATCAACCATAA	:	857
Staph	:	ACCGTTCTAGTTCAAGGCCTTTGGCAAACATGACGA	:	920
E.coli	:	ACCGTTCTAGTTTACTGGCTTGGTGGTCATGAAGA	:	918
Sal	:	GCCTTTCTATTTCACCGGCTTCGGACGTCATGAAGA	:	893
Staph	:	CAGTCCTATCAACGGGCGTGGCTTAAACGAAGCGAG	:	956
E.coli	:	TGCGGACTTACGTGGCAAAGGATTGATAAGGTGGT	:	954
Sal	:	TGCGGACTTGGCGCGTAAGGCTTTGATAACGTGGT	:	929
Staph	:	CAATGTGATGGATTTCAATATCCTCAAATGGATCGG	:	992
E.coli	:	GATGGTGGAGGACCAAGCATTAATGGACTGGATTGG	:	990
Sal	:	GATGGTGGAGGACCAAGCGCTAATGGACTGGATCGG	:	965
Staph	:	GCGGAACAGCTTCCGGACCGCACACTATCCGTACTC	:	1028
E.coli	:	GGCGAAGCTCGTACCGTACCTCGCATTAACCTTACGC	:	1026
Sal	:	TGCGAAGCTTTACCGTACCTCGCATTAACCTTATGC	:	1001
Staph	:	TGAAGAGTTGATGGCTCTTCCGGATCGCGAGGGTCT	:	1064
E.coli	:	TGAAGACATGCTCGACTGGGCAAGATGAAGATGGCAT	:	1062
Sal	:	GGAAGACATGCTCGACTGGGCGGACGAACATGGCAT	:	1037
Staph	:	GGTGGTGATCGACGAGACTCCGGCACTTGGGGTGCA	:	1100
E.coli	:	CGTGGTGATTGATGAAGCTGCTGCTGTGGGGTTTAA	:	1098
Sal	:	CGTCATCATTGATGAAGACGGCCGGCCGTGGGATTCAA	:	1073
Staph	:	CCTGAAGTTTATCGCCACACGGGACTCGGGCGAAGG	:	1136
E.coli	:	CCCTCTTTTAGGCATTGGTTTGAAGCGGGCAACAA	:	1134
Sal	:	CCTGTCTTTTAGGCATTAGCTTTGATGTGGGCGAAAA	:	1109

FIG. 19D

Staph : ---GAGCGAGCGGGTCAGTACCTGGGAGAAATTCC : 1169
 E.coli : GCGGAAAGAACTGTACAGCGAAGAGGGCAGTCAACGG : 1170
 Sal : ACCCAAGAGACTCTACAGCGATCAGGCCCTGAAAGGA : 1145

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Staph : GACGTTTCAGCAC---CATCAAGACGTTCTCCGTGA : 1202
 E.coli : CGAAACTCAGCAAGCCGACGTTAGACCCGATTAAAGA : 1206
 Sal : TCAAACCGAGCGCGGCGAGCTCGAGGCAATTAAAGGA : 1181

Staph : ACTGCTGTCTCGTGAGAAAGAACCATCCAAGCGTCGT : 1238
 E.coli : CCTGATAGCGCGTGAGAAAGAACCATCCAAGCGTCGT : 1242
 Sal : GCTGATTGCCCGCGATAAGAACCATCCAAGCGTCGT : 1217

Staph : GATGTGGACCATCGCCAACGAGCGCGGACTGAGGA : 1274
 E.coli : GATGTGGACATATCGCCAACGAGCGGATACCCGTCG : 1278
 Sal : CATGTGGACATATCGCCAACGAGCGGATACCCGCGG : 1253

Staph : AGAGCGGCGCTACGACTAGTTCAAGCCGTTGGTCCA : 1310
 E.coli : CCA-AGTGCAGCGGATATTTTCG--CCACTGGCGGA : 1311
 Sal : GAACGCGCGCGCGGAATAGTTCCCTCCGCTGGCGCA : 1289

Staph : CCTGACCAAGCAACTCGAGCCACAGAGCGTCCGGT : 1346
 E.coli : AGCAACGCGGTAAACTCGAGCC---GACGCGTCCGAT : 1344
 Sal : GCGAACGCGCGCAACTCGATCC---TACAGCTCCGAT : 1322

Staph : GACGATCGTCTGTCTGATGGCTACCCCGGAGAC : 1382
 E.coli : CACGTGCGTCAATGTAATGTTCTGGGACGCTCACAC : 1380
 Sal : AACCTGCGTGAACGTTGTTCTGCGATGCGGAAAG : 1358

Staph : GGAGAAAGTCCCGCAACTGATTGACGTCATCGCGCT : 1418
 E.coli : CGATACCATCAGCGATCTCTTTGATGTGCTGGGCT : 1416
 Sal : CGACACCATTAACCGAATCTCTTTGATGTCGTTGGCT : 1394

FIG. 19E

Staph : CAAATCGGTATAACGGATGGTACTTGGATCGCCGGTGA : 1434
E.coli : GAACCGGTATTACGGATGGTATGTCCAAAGCGGCCGA : 1452
Sal : GAACCGGTACTACGGCTGGTATGTACAAAGCGGCCGA : 1430

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Staph : TCTCGAAGCGGCCAAAGTCCATCTCCGCCAGGAATT : 1490
E.coli : TTTGGAAACGGGCACAGAGGTACTGGAAAAAGAACT : 1488
Sal : TCTGGAGAAGGCTCAGAAAGTCTGGAGAAAGAGCT : 1466

Staph : TCACGCGTGGAAACAACCGTTGCCAGGAAAGCCGAT : 1526
E.coli : TCTGGCCTGGCAGGACAAAGTGC---ATCAGCCGAT : 1521
Sal : TCTGCGCTGGCAGGACAAAGTGC---ACGCGCCGAT : 1499

Staph : CATCATCACTGACTACGCCGCAGACACCGTTGCCGG : 1562
E.coli : TATCATCACCGAATACGGCGTGGATACGTTAGGGGG : 1557
Sal : TATCATCACCGAATACGGCGTGGATACGTTGCCAGG : 1535

Staph : GTTTCAGGACATTGATCAGTGATGTTCAACCGAGGA : 1598
E.coli : GCTGGCACTCAATGTACACCGACATGTCCAGTGAAGA : 1593
Sal : CCGTGCATTCCATGTACAAAGATATGTGGAGCGAAGA : 1571

Staph : ATATCAAGTCCAGTACTACCGGGCGAAGCAGGTCGT : 1634
E.coli : GTATCAGTGTGCATGGCTCGATATGATCACCGCGT : 1629
Sal : GTACCAGTGGCGCTGGCTTGATATGTACCATCGCGT : 1607

Staph : GTTCCATGAGTTTGAGAACTTCGTGGCTGAGCAAGC : 1670
E.coli : CTTTGATCGCGTCAGCGCCGTCTGTCCGTCGAACAGCT : 1665
Sal : GTTTCATCGCGTCAGCGCCGTCTGTCCGTCAGCAGGT : 1643

Staph : GTGGAAGTTCCGCCGACTTGGCGACCTCTCAGGCCCT : 1706
E.coli : ATGGAATTTCGCCGATTTTGGCGACCTCGCAAGGCAT : 1701
Sal : ATGGAAGTTCCGCCGACTTGGCGACCTTCGCAGGGCAT : 1679

FIG. 19F

Figure 19G

Staph	:	GATGCGCGTCCAAGCAACAAGAACGGCGTGTTTAC	:	1742
E.coli	:	ATTGCGCGTTGGCGGTACAAGAAACGGATCTTCAC	:	1737
Sal	:	TATGCGCGTTGGCGGCAACAAAAAGGTATATTAC	:	1715
Staph	:	TCGTGACCGCAAGCCGAAGCTCGCCGGCAGGCTCT	:	1778
E.coli	:	TCGGGACCGCAAAACCGAAGTCGGCGGGCTTTCTGGCT	:	1773
Sal	:	CCGGGACAGAAAAACCAAAATCGGCGGGCTTCTGGCT	:	1751
Staph	:	TCGCGAGCGCTGGACCAACATTCCACATTTCGGCTA	:	1814
E.coli	:	GCAAAAACGCTGGACTGGCAT---GAAGTTCGGTGA	:	1806
Sal	:	GCAAAAACGCTGGACCGGCAT---GGACTTTGGCGT	:	1784
Staph	:	CAAGAA	:	1821
E.coli	:	AAAAGCGCAGCAGGGAGGCAAACAATGAATCAACAA	:	1842
Sal	:	GAAGCCCAGCAGGGAGATAAATAATGA	:	1812
Staph	:	-----	:	-
E.coli	:	CTCTCCTGGCGCACCATCGTCCGGCTACAGCCTCGGT	:	1878
Sal	:	-----	:	-
Staph	:	-----	:	-
E.coli	:	GACGTCGCCAATAACTTCGCCTTCGCAATGGGGGCG	:	1914
Sal	:	-----	:	-
Staph	:	-----	:	-
E.coli	:	CTCTTCCTGTTGAGTTACTACACCGACGTCGCTGGC	:	1950
Sal	:	-----	:	-
Staph	:	-----	:	-
E.coli	:	GTCGGTGCCGCTGCGGCGGGCACCATGCTG	:	1980
Sal	:	-----	:	-

FIG. 19G